



# Replacement Sheet

Figure 3A

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned. Alignment Score = 118839  
Gaps Inserted = 0 Conserved Identities = 936

Pairwise Alignment Mode: Fast  
Pairwise Alignment Parameters:  
ktup = 1 Gap Penalty = 3 Top Diagonals = 5 Window Size = 5

Multiple Alignment Parameters:  
Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1  
Delay Divergent = 40% Gap Distance = 8  
Similarity Matrix: blosum

Processing time: 12.9 seconds

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Spy74_M3      1                               DYAES      5
Spy70_M5      1          LVKEPILKQTQASSSISGADYAES    24
Spy69_M6      1                               KQTQASSSISGADYAES    17
Spy68_M2      1          LVKEPILKQTQASSSISGADYAES    24
Spy60_M1      1          LVKEPILKQTQASSSISGADYAES    24
12357_M18     1          VKEPILKQTQASSSISGADYAES    23
700294_M1     1 MKKHLKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES    50
                                     *****

Spy74_M3      6 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    55
Spy70_M5     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    74
Spy69_M6     18 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    67
Spy68_M2     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    74
Spy60_M1     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    74
12357_M18    24 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    73
700294_M1    51 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    100
      *****

Spy74_M3     56 ENTESEKQITSGSQLEQSKESLSLNKRV PSTSNWEICDFITKGNTLVGLS    105
Spy70_M5     75 ENTESEKQINSGSQLEQSKESLSLNKRV PSTSNWEICDFITKGNTLVGLS    124
Spy69_M6     68 ENTESEKQINSGSQLEQSKESLSLNKRV PSTSNWEICDFITKGNTLVGLS    117
Spy68_M2     75 ENTESEKQITSGSQLEQSKESLSLNKTV PSTSNWEICDFITKGNTLVGLS    124
Spy60_M1     75 ENTESEKQITSGSQLEQSKESLSLNKTV PSTSNWEICDFITKGNTLVGLS    124
12357_M18    74 ENTESEKQINSGSQLEQSKESLSLNKRV PSTSNWEICDFITKGNTLVGLS    123
700294_M1   101 ENTESEKQITSGSQLEQSKESLSLNKTV PSTSNWEICDFITKGNTLVGLS    150
      *****

Spy74_M3     106 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    155
Spy70_M5     125 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy69_M6     118 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    167
Spy68_M2     125 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy60_M1     125 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
12357_M18    124 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    173
700294_M1    151 KSGVEKLSQTDHLVLP SQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    200
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## Replacement Sheet

Figure 3B

Spy74_M3	156	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	205
Spy70_M5	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy69_M6	168	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	217
Spy68_M2	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy60_M1	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
12357_M18	174	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	223
700294_M1	201	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	250
*****			
Spy74_M3	206	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	255
Spy70_M5	225	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	274
Spy69_M6	218	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	267
Spy68_M2	225	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	274
Spy60_M1	225	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	274
12357_M18	224	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	273
700294_M1	251	EVNLPESLETISDYAFAHLALKQIDLDPNLKAIGELAFFDNQITGKLSLP	300
*****			
Spy74_M3	256	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	305
Spy70_M5	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy69_M6	268	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	317
Spy68_M2	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy60_M1	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
12357_M18	274	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	323
700294_M1	301	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	350
*****			
Spy74_M3	306	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	355
Spy70_M5	325	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy69_M6	318	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	367
Spy68_M2	325	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy60_M1	325	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	374
12357_M18	324	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	373
700294_M1	351	IESEAFNGPNPGDDHYNRRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	400
*****			
Spy74_M3	356	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	405
Spy70_M5	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	424
Spy69_M6	368	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	417
Spy68_M2	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	424
Spy60_M1	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	424
12357_M18	374	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	423
700294_M1	401	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRKNKNLEIPKQHNGVTITEI	450
*****			
Spy74_M3	406	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	455
Spy70_M5	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy69_M6	418	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	467
Spy68_M2	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy60_M1	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
12357_M18	424	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	473
700294_M1	451	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	500
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# Replacement Sheet

## Figure 3C

Spy74_M3	456	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	505
Spy70_M5	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy69_M6	468	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	517
Spy68_M2	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy60_M1	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
12357_M18	474	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	523
700294_M1	501	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	550
*****			
Spy74_M3	506	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	555
Spy70_M5	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy69_M6	518	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	567
Spy68_M2	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy60_M1	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
12357_M18	524	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	573
700294_M1	551	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	600
*****			
Spy74_M3	556	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	605
Spy70_M5	575	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	624
Spy69_M6	568	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	617
Spy68_M2	575	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	624
Spy60_M1	575	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	624
12357_M18	574	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	623
700294_M1	601	SDNALKEVLLPASLKTIREEAFFKKNHLKQLEVASALS HIAFNALDDNDGD	650
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Spy74_M3	606	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILK LIEGLDY	655
Spy70_M5	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	674
Spy69_M6	618	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	667
Spy68_M2	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMIDLEKILK LIEGLDY	674
Spy60_M1	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	674
12357_M18	624	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	673
700294_M1	651	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	700
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Spy74_M3	656	STLRQTTQTQFRDMTTAGKALLSKSKLRQGEKQKFLQEAQFFLGRVDL DK	705
Spy70_M5	675	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	724
Spy69_M6	668	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	717
Spy68_M2	675	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	724
Spy60_M1	675	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	724
12357_M18	674	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	723
700294_M1	701	STLRQTTQTQFRDMTTAGKALLSKSKNL RQGEKQKFLQEAQFFLGRVDL DK	750
*****			
Spy74_M3	706	AIAKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	755
Spy70_M5	725	AIAKAEKALVTKKATKNGQLLRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy69_M6	718	AIAKAEKALVTKKATKNGQLLRSINKAVSAYNNSAIKKANVKRLEKELD	767
Spy68_M2	725	AIAKAEKALVTKKATKNGQLLRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy60_M1	725	AIAKAEKALVTKKATKNGQLLRSINKAVLAYNNSAIKKANVKRLEKELD	774
12357_M18	724	AIAKAEKALVTKKATKNGQLLRSINKAVLAYNNSAIKKANVKRLEKELD	773
700294_M1	751	AIAKAEKALVTKKATKNGQLLRSINKAVLAYNNSAIKKANVKRLEKELD	800
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# Replacement Sheet

## Figure 3D

Spy74_M3	756	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	805
Spy70_M5	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy69_M6	768	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	817
Spy68_M2	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy60_M1	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
12357_M18	774	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	823
700294_M1	801	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	850
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Spy74_M3	806	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	855
Spy70_M5	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
Spy69_M6	818	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	867
Spy68_M2	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
Spy60_M1	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
12357_M18	824	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	873
700294_M1	851	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	900
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Spy74_M3	856	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	905
Spy70_M5	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKAGTHSEKSSSS	924
Spy69_M6	868	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	917
Spy68_M2	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGMHSEKSSSS	924
Spy60_M1	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	924
12357_M18	874	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	923
700294_M1	901	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	950
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Spy74_M3	906	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	951
Spy70_M5	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	970
Spy69_M6	918	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	963
Spy68_M2	925	ESANSKDRGLQSHPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL	971
Spy60_M1	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL	971
12357_M18	924	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	969
700294_M1	951	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALLSLI	1000
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Spy74_M3	952	951
Spy70_M5	971	970
Spy69_M6	964	963
Spy68_M2	972	971
Spy60_M1	972	971
12357_M18	970	969
700294_M1	1001	TAIKKKKY 1008